

SEQUENCE LISTING

<110> Sundstrom, Paula

<120> METHODS AND COMPOSITIONS FOR REGULATING BUD-HYPHA TRANSITIONS AND CAMP LEVELS BY THE ADENYLATE CYCLASE-ASSOCIATED PROTEIN GENE, CAP

<130> 48544.00012

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 545

<212> PRT

<213> Candida albicans

<400> 1

```

Met Ser Thr Glu Glu Ser Gln Phe Asn Val Gln Gly Tyr Asn Ile Ile
1      5      10      15
Thr Ile Leu Lys Arg Leu Glu Ala Ala Thr Ser Arg Leu Glu Asp Ile
20     25     30
Thr Ile Phe Gln Glu Glu Ala Asn Lys Asn His Tyr Gly Val Asp Ser
35     40     45
Leu Thr Glu Lys Gly Thr Pro Lys Ser Arg Thr Val Glu Ser Ser Glu
50     55     60
Ala Thr Ser Asp Gly Lys Ser Leu Glu Ser Thr Ser Phe Ala Thr Phe
65     70     75     80
Ser Glu Ala Pro Val Glu Lys Ser Lys Leu Ile Val Glu Phe Glu Asn
85     90     95
Phe Val Glu Ser Tyr Val His Pro Leu Val Glu Thr Ser Lys Lys Ile
100    105    110
Asp Ser Leu Val Gly Glu Ser Ala Gln Tyr Phe Tyr Glu Ala Phe Val
115    120    125
Glu Gln Gly Lys Phe Leu Glu Leu Val Leu Gln Ser Gln Gln Pro Asp
130    135    140
Met Thr Asp Pro Ala Leu Ala Lys Ala Leu Glu Pro Met Asn Ala Lys
145    150    155    160
Cys Thr Lys Ile Asn Glu Leu Lys Asp Ser Asn Arg Lys Ser Pro Phe

```

165										170					175				
Phe	Asn	His	Leu	Ser	Thr	Phe	Ser	Glu	Ser	Asn	Ala	Val	Phe	Tyr	Trp				
			180					185					190						
Ile	Gly	Ile	Pro	Thr	Pro	Val	Ser	Tyr	Ile	Thr	Asp	Thr	Lys	Asp	Thr				
		195					200					205							
Val	Lys	Phe	Trp	Ser	Asp	Arg	Val	Leu	Lys	Glu	Tyr	Lys	Thr	Lys	Asp				
	210					215					220								
Gln	Val	His	Val	Glu	Trp	Val	Lys	Gln	Thr	Leu	Ser	Val	Phe	Asp	Glu				
225					230					235					240				
Leu	Lys	Asn	Tyr	Val	Lys	Glu	Tyr	His	Thr	Thr	Gly	Val	Ala	Trp	Asn				
				245					250					255					
Pro	Lys	Gly	Lys	Pro	Phe	Ala	Glu	Val	Val	Ser	Gln	Gln	Thr	Glu	Ser				
			260					265					270						
Ala	Ala	Lys	Asn	Ser	Ser	Ser	Ala	Ser	Gly	Ser	Ala	Gly	Gly	Ala	Ala				
		275					280					285							
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Thr	Phe	Phe	Asp	Asp	Thr				
	290					295					300								
Glu	Lys	Asp	Ser	Glu	Asn	Pro	Ser	Pro	Ala	Ser	Gly	Gly	Ile	Asn	Ala				
305					310					315					320				
Val	Phe	Ala	Glu	Leu	Asn	Gln	Gly	Ala	Asn	Ile	Thr	Ser	Gly	Leu	Lys				
				325					330					335					
Lys	Val	Asp	Lys	Ser	Glu	Met	Thr	His	Lys	Asn	Pro	Glu	Leu	Arg	Lys				
			340					345					350						
Gln	Pro	Pro	Val	Ala	Pro	Lys	Lys	Pro	Ala	Pro	Pro	Lys	Lys	Pro	Ser				
		355					360					365							
Ser	Leu	Ser	Gly	Gly	Val	Ser	Ser	Ala	Pro	Val	Lys	Lys	Pro	Ala	Lys				
	370					375					380								
Lys	Glu	Leu	Ile	Asp	Gly	Thr	Lys	Trp	Ile	Ile	Gln	Asn	Phe	Thr	Lys				
385					390					395					400				
Ala	Asp	Ile	Ser	Asp	Leu	Ser	Pro	Ile	Thr	Ile	Glu	Val	Glu	Met	His				
				405					410					415					
Gln	Ser	Val	Phe	Ile	Gly	Asn	Cys	Ser	Asp	Val	Thr	Ile	Gln	Leu	Lys				
			420					425					430						
Gly	Lys	Ala	Asn	Ala	Val	Ser	Val	Ser	Glu	Thr	Lys	Asn	Val	Ala	Leu				
		435					440					445							
Val	Ile	Asp	Ser	Leu	Ile	Ser	Gly	Val	Asp	Val	Ile	Lys	Ser	Tyr	Lys				
	450					455					460								
Phe	Gly	Ile	Gln	Val	Leu	Gly	Leu	Val	Pro	Met	Leu	Ser	Ile	Asp	Lys				
465					470					475					480				
Ser	Asp	Glu	Gly	Thr	Ile	Tyr	Leu	Ser	Gln	Glu	Ser	Ile	Asp	Asn	Asp				
				485					490					495					
Ser	Gln	Val	Phe	Thr	Ser	Ser	Thr	Thr	Ala	Leu	Asn	Ile	Asn	Ala	Pro				
			500					505					510						
Lys	Glu	Asn	Asp	Asp	Tyr	Glu	Glu	Leu	Ala	Val	Pro	Glu	Gln	Phe	Val				
		515					520					525							

Ser Lys Val Val Asn Gly Lys Leu Val Thr Gln Ile Val Glu His Ala
 530 535 540

Gly
 545

<210> 2

<211> 1634

<212> DNA

<213> *Candida albicans*

<400> 2

```

atgtcaaccg aggagagtca attcaatggt caagggtaca atattatcac aatcttgaaa      60
agattagagg cagcaacgtc tcgtcttgag gacattacca tttccaaga ggaagcaaac      120
aaaaaccaca tggagttgat tctctcactg aaaaggggaa ccccaaaagc agaactgttg      180
aatcgtcaga agcaacttcc gatggtaaat cactcgaatc tacatcattt gccacttttt      240
ctgaagctcc tgtagaaaaa tccaaattga ttgtggaatt tgagaacttt gttgaaagct      300
acgttcatcc acttgttgaa acatccaaaa agatcgattc cttggtgggg gagtccgccc      360
aatattttta tgaggcattt gtcgaacaag ggaaatTTTT ggagcttgta ttgcaatccc      420
aacaaccaga tatgactgat ccagctttgg caaaggcatt agaaccaatg aatgctaaat      480
gcacaaaaat taacgaatta aaaattccaa tcgtaaatct ccattcttca atcatttaag      540
cactttcagt gaaagtaatg ccgtttttta ttggattggg atccctacac cagtctcgta      600
cattactgat actaaagata cagtcaaatt ttggtctgac agagttttaa aagaatacaa      660
gaccaaagac caagtgcatt ttgaatgggt aaaacaaaca ttatctgttt ttgacgaatt      720
gaagaattat gttaaagaat atcacacaac tgggtgttgct tggaacccca aaggaaagcc      780
ttttgcagaa gttgtatctc agcaaacaga gagtgctgct aagaattctt cgtctgcttc      840
tggttctgca ggaggagcag ctccaccacc acctccacct ccacctccag caacgttttt      900
tgatgacact gaaaaagaca gtgaaaatcc atctcagctt cagggtggtat taatgcgggt      960
ttgttgaatt gaatcaagggt gccaacatca catctggttt aaaaaaagtc gacaaatctg     1020
agatgacgca taagaaccct gaattaagaa aacagccacc agttgcacca aaaaaaccag     1080
caccaccaaa gaagccatct agtttatccg gtggtgtgag ttcagctcca gtaaagaagc     1140
ctgctaagaa ggagttgatt gacggtacaa aatggataat tcaaaatTTT acaaaagctg     1200
atatttccga tttgagtcca attaccattg aagttgagat gcatcaatct gttttcattg     1260
gtaattgtag tgatgtcacc attcagttga aaggtaaagc aaatgcagtg tcggtatcgg     1320
aaaccaagaa tgtggctctt gtcattgatt cgttgatttc cggagtcgat gttattaaat     1380
cctacaagtt tggatataca gttttaggtt tgggtaccaat gttgagtatt gataaatcag     1440
atgaagggac tatctatttg tcgcaagaaa gcattgacaa tgatagtcag gtttttacta     1500
gtagcactac agcactcaac atcaatgcac caaaggaaaa tgatgattat gaagaattgg     1560

```

ctgttcctga acaatttggt agtaagggtg tgaatggcaa attagtcact caaattgttg 1620
aacatgctgg ataa 1634

SEQ ID NO. 8
PDE2 amino acid sequence

MAEVLSLVDLEIPQVTDKYYKFDTFKHLICHLFKKTSTETDSNV
PIVIFPTNNDIPSRKTRSTTTTTTTTTNTSKLDNLPFSDKSLLIQFFFTHLNILM
IQGENSDEGKLYQEISSAKELLNTRISRVGNWTGTTFRYCRHENDCGLLNQHSKIAG
IIPMTYILNCNATRSEIATNQLIYLRMIEEINFIELLQDASTTRLSQLCYAVGHW
SFAHNLSNDDLVCVYLMIDYAIKQVEGFDNIPLNELLAFFIVRDTYKNGNPFHNF
RHAVDVLQACFHLIRLGLSLPKFKQFVEDPKLDYTEVHDTHTVLIALQNSSEEKASL
NPIQTLGLLVAALGHDVGHGPGTTNDFMIKFSAPTALLYNDRSVLESYHASLFINKVLR
ICWPDLLTCTIEEKSELTIRSLIISILATDMGEHNEYVNRKLSFKTHNEILNHDNTV
KLISALLIKCADISNVTRPLRVSAQWAMVLSREFAEVELLSVIKKDIDLDFTKDLTY
DDVPHELREILEIQPDIHKQIIFINLFAENLFNSVSDLLPQLQYTCDIIMENKLFWL

SEQ ID NO. 9

Genbank accession number CAA21984 for PDE2

1 maevlslvds eipqvtdkyy kfdtfkhlic hlfkktstet dsnvpiviif ptnndipsrk
61 trsttttttt attntskld nlpfsdksll iqffffthlni lmiqgensde gklyqeissa
121 kelltnrisr vgnwtgtthf ryrhendcg llmqhskiag iptmttyiln cnatrseiat
181 nqliylyrlm ieeinfiell qdasttrlsq lcyavghwsf pahnlsnddl vvcvylmidv
241 aikqvegfdn iplnellafi fivrtdtykng npfhnrhav dvlqacfhfl irlgslpkfk
301 qfvedpkldy tevhdktvl ialqnssee kaslnpiqt1 glvaalghd vghpgttndf
361 mikfsapta1 lyndrsvles yhaslfinkv lricwpdllt ctieekselt irsliissil
421 atdmgehney vnrlksfkth neilnhdntv klisallikc adisnvtrpl rvsaqwamv1
481 srefaevell ksvikkdirl dftkdldtydh vphelreile iqpdihkgqi ffinlfaen1
541 fnsvsdllpq lqytcdiime nk1fwlerak k

SEQ ID. NO. 10

tttttttatt t

SEQ ID NO. 13

PDE2 cDNA sequence

1 atggcagaag tattatcatt gggtgacctc gagattcctc aagtcactga taagtattat
61 aaatttgaca cttttaaaca tttaatctgt cacttggtca agaaaaccag cacagaaact
121 gattcaaagt ttcctatagt aataatattc cgcaccaaca atgatatccc ttcgagaaag
181 actcgatcta ctactaccac caccactact actactacta ctaataccag caagttagac
241 aatttgccat tcagtataaa atcgttggtg atacaattct tcttcaccca tttgaacata
301 ttgatgattc aaggagagaa ttcggatgag ggaaagtatt atcaagaaat aagttcagcc
361 aaagaattat tgacaaatag gatatacaga gttggaaatt ggacaggaac aactcatttt
421 agatactgtc gacatgagaa tgattgtgga ctattgaatc aacattccaa aattgcagga
481 attataccca caatgactta cattctcaat tgtaatgcaa caagatcaga aattgccact
541 aaccaattga tatatttata tcgactcatg atagaggaga ttaattttat tgaattgtta
601 caagatgcac ctacgacaag attatctcag ttgtgttatg ctgtgggaca ttggagtctc
661 cctgtcctata atttatcaaa tgacgatttg gtttattgtg tttatttgat gatagattac
721 gctatcaaac aagttgaagg gtttgacaac attcctttga atgaattatt ggcatttata
781 tttattgtta gagataccta taagaatggg aatccgttcc ataatttccg ccacgctgtg
841 gatgttctac aagcttggtt ccatttttct attagattgg gtagtttacc caaattcaag
901 caatttgctg aggaccgaa attggattac accgaagttc atgacacaca tactgtattg
961 attgccttac aaaacaattc ctccgaggaa aaagcttctc ttaatccaat acaaacatta
1021 ggggttattgg ttgcagcatt gggccatgat gtgggcccac caggtacgac aaatgatttc
1081 atgattaaat tcagtgcacc aacggcacta ctttacaatg acagatctgt tcttgaatct
1141 tatcatgcat ctttatttat caataaagt ttaagaatat gttggccaga tttattaact
1201 tgtacaattg aggaaaaatc agagttaacc attagaagtt tgataatttc ttcgatattg

1261	gccaccgata	tgggtgaaca	taatgaatat	gttaatcggg	tgaaatcttt	caagacccat
1321	aatgaaat	taaaccatga	taacactggt	aaattgattt	ctgccttggt	aatcaa
1381	gctgatattt	ctaacgtgac	gagaccggtg	agagtatctg	cacaatgggc	aatgggttta
1441	tcaagagaat	ttgcagaagt	tgagttgctc	aaatcggtaa	tcaaaaaaga	tattgatctt
1501	gactttacca	aagatttaac	ttatgatgat	gttccacatg	aattacgcga	aatacttgaa
1561	atacaacccg	atatacataa	aggacagata	ttttcatca	atttattcgc	tgagaattta
1621	tttaatatg	ttagtgattt	attacctcaa	ttgcagtata	cttgtgat	tattatggaa
1681	aacaaactat	tttggttgga	aagagcaaag	aaataa		